BIOTECHNOLOGY
SYSTEMS
BRANCH

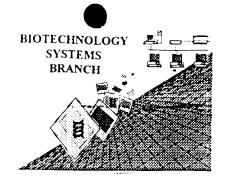# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,756

Source: OIPE

Date Processed by STIC: 10/4/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker and is ST.25 compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/620,756_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules
Please ensure your subsequent submission is saved in ASCII text so that it can be processed

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing If intentional, please use the following format for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES." response to include the skipped sequence(s)

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence
<210> sequence id number
<400> sequence id number
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10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing
Use of <220> to <223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response

_____ ___ <220>Feature (NEW RULES)
Sequence(s) _____ ____
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. T_____ ____
the resulting a_____ ____ by n___ ____ bottlenecks responses (as well ____ ____ ____ ____
Instead, please use "File Manager" or any other means to copy file to floppy disk

OIPE

P.6

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION   US/09/670,756   TIME: 22:17:51

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

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  3  <110> APPLICANT: Rhodes, Kenneth
  4         Betty, Maria
  5         Ling, Huai-Ping
  6         An, Wenqian
  8  <120> TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
 10  <130> FILE REFERENCE: MNI-010CP1
 12  <140> CURRENT APPLICATION NUMBER: US/09/670,756
 13  <141> CURRENT FILING DATE: 2000-09-27
 15  <150> PRIOR APPLICATION NUMBER: USSN 60/110,277
 16  <151> PRIOR FILING DATE: 1998-11-30
 18  <150> PRIOR APPLICATION NUMBER: USSN 60/110,033
 19  <151> PRIOR FILING DATE: 1998-11-25
 21  <150> PRIOR APPLICATION NUMBER: USSN 60/109,333
 22  <151> PRIOR FILING DATE: 1998-11-20
 24  <150> PRIOR APPLICATION NUMBER: USSN 09/298,731
 25  <151> PRIOR FILING DATE: 1999-04-23
 27  <150> PRIOR APPLICATION NUMBER: USSN 09/350,614
 28  <151> PRIOR FILING DATE: 1999-07-09
 30  <150> PRIOR APPLICATION NUMBER: USSN 09/350,874
 31  <151> PRIOR FILING DATE: 1999-07-09
 33  <150> PRIOR APPLICATION NUMBER: USSN 09/400,492
 34  <151> PRIOR FILING DATE: 1999-09-21
 36  <150> PRIOR APPLICATION NUMBER: USSN 09/399,913
 37  <151> PRIOR FILING DATE: 1999-09-21
 39  <150> PRIOR APPLICATION NUMBER: PCT/US99/27428
 40  <151> PRIOR FILING DATE: 1999-11-19
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 54  <222> LOCATION: (225)..(872)
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 62  ttttctctcc tccaattcag agtagacaaa ccacggggat ttctttccag ggtaggggag 180
 64  gggccgggcc cggggtccca actcgcactc aagtcttcgc tgcc atg ggg gcc gtc 236
 65                                                   Met Gly Ala Val
 66                                                    1
 68  atg ggc acc ttc tca tct ctg caa acc aaa caa agg cga ccc tcg aaa   284
 69  Met Gly Thr Phe Ser Ser Leu Gln Thr Lys Gln Arg Arg Pro Ser Lys
 70   5              10               15              20
 72  gat aag att gaa gat gag ctg gag atg acc atg gtt tgc cat cgg ccc   332
 73  Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro
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RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION   US/09/670,756   TIME: 22:17:51

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Output Set: N:\CRF3\10042000\I670756.raw

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78           40              45                    50
80 ctg cag gtc ctt tat aga ggc ttc aaa aat gag tgc ccc agt ggt gtg   428
81 Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val
82           55              60                    65
84 gtc aac gaa gac aca ttc aag cag atc tat gct cag ttt ttc cct cat   476
85 Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His
86           70              75                    80
88 gga gat gcc agc acg tat gcc cat tac ctc ttc aat gcc ttc gac acc   524
89 Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr
90    85              90              95                    100
92 act cag aca ggc tcc gtg aag ttc gag gac ttt gta acc gct ctg tcg   572
93 Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
94           105             110                   115
96 att tta ttg aga gga act gtc cac gag aaa cta agg tgg aca ttt aat   620
97 Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn
98           120             125                   130
100 ttg tat gac atc aac aag gac gga tac ata aac aaa gag gag atg atg   668
101 Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met
102          135             140                   145
104 gac att gtc aaa gcc atc tat gac atg atg ggg aaa tac aca tat cct   716
105 Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro
106    150             155              !        160
108 gtg ctc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag   764
109 Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln
110 165             170              175                   180
112 aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt   812
113 Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu
114          185             190                   195
116 gaa tca tgt cag gag gac gac aac atc atg agg tct ctc cag ctg ttt   860
117 Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe
118          200             205                   210
120 caa aat gtc atg taactggtga cactcagcca ttcagctctc agagacattg   912
121 Gln Asn Val Met
122          215
124 tactaaacaa ccaccttaac accctgatct gcccttgttc tgattttaca caccaactct   972
126 tgggacagaa acacctttta cactttggaa gaattctctg ctgaagactt tcttatggaa  1032
128 cccagcatca tgtggctcag tctctgattg ccaactcttc ctctttcttc ttcttgagag  1092
130 agacaagatg aaatttgagt ttgtttggaa agcatgctca tctcctcaca ctgctgccct  1152
132 atggaaggtc cctctgctta agcttaaaca gtagtgcaca aaatatgctg cttacgtgcc  1212
134 cccagcccac tgcctccaag tcaggcagac cttggtgaat ctggaagcaa gaggacctga  1272
136 gccagatgca caccatctct gatggcctcc caaaccaatg tgcctgtttc tcttcctttg  1332
138 gtgggaagaa tgagagttat ccagaacaat taggatctgt catgaccaga ttgggagagc  1392
110 cagcacctaa catatgtggg ataggactga attattaagc atgacattgt ctgatgaccc  1452
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146 <211> LENGTH: 216
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155             20                  25                  30
157 Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
158         35                  40                  45
160 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
161     50                  55                  60
163 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
164   65                  70                  75                  80
166 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
167             85                  90                  95
169 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
170             100                 105                 110
172 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
173         115                 120                 125
176 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
177     130                 135                 140
179 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
180 145                 150                 155                 160
182 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
183             165                 170                 175
185 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
186             180                 185                 190
188 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
189         195                 200                 205
191 Leu Gln Leu Phe Gln Asn Val Met
192     210                 215
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 1856
197 <212> TYPE: DNA
198 <213> ORGANISM: Rattus sp.
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (300)..(1034)
204 <400> SEQUENCE: 3
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209 ggggaaataa aagcaaagat taccatgaat tgcaagatta cctagcaatt gcaaggtagg 180
211 aggagagagg tggagggcgg agtagacagg agggagggag aaagtgagag gaagctaggc 240
213 tggtggaaat aaccctgcac ttggaacagc ggcaaagaag cgcggatttc cagctttaa 299
215 atg cct gcc cgc gtt ctg ctt gcc tac ccg gga acg gag ata ttg acc   347
216 Met Pro Ala Arg Val Leu Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
217   1               5                  10                  15
219 cag ggc gag tct gaa ggg ctc cag acc ttg gga ata gta gta gtc ctg   395
220 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
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RAW SEQUENCE LISTING   DATE: 10/04/2000
PATENT APPLICATION   US/09/670,756   TIME: 22:17:54

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Output Set: N:\CRF3\10042000\I670756.raw

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223 tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gac ttg tca   445
224 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
225         35              40              45
227 gat gac aag atc gag gat gat ctg gag atg acc atg gtt tgc cat cgg   491
228 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
229     50              55              60
233 cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc aag aga   539
234 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
235  65              70              75              80
237 gaa ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt   587
238 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
239             85              90              95
241 gtg gtt aac gaa gag aca ttc aag cag atc tac gct cag ttt ttc cct   635
242 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
243             100             105             110
245 cat gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac   683
246 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
247         115             120             125
249 acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act gct ctg   731
250 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
251     130             135             140
253 tcg att tta ctg aga gga acg gtc cat gaa aaa ctg agg tgg acg ttt   779
254 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
255 145             150             155             160
257 aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg   827
258 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
259             165             170             175
261 atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat   875
262 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
263             180             185             190
265 cct gtg ctc aaa gag gac act ccc agg cag cac gtg gac gtc ttc ttc   923
266 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
267         195             200             205
269 cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gac gaa ttt   971
270 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
271     210             215             220
273 ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg   1019
274 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
275 225             230             235             240
277 ttc caa aat gtc atg taactgagga cactggccat cctgctctca gagacactga   1074
278 Phe Gln Asn Val Met
279             245
281 caaacacctc aatgccctga tctgcccttg ttccagtttt acacatcaac tctcgggaca   1134
283 gaaatacctt ttacactttg gaagaattct ctgctgaaga ctttctacaa aacctggcac   1194
285 cgagtggctc agtctctgat tgccaactct tcctccctgc tcctcttgag agggacgagc   1254
287 tgaaatccga agtttgtttt ggaagcatgc ccatctctcc atgctgctgc tgccctgtgg   1314
289 aaggcccctc tgcttgagct taaacagtag tgcacagttt tctacgtata cagatcccca   1374
291 actcactgcc tctaagtcag gcagaccctg atcaatctga accaaatgtg caccatcctc   1434
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293 cgatggcctc ccaagccaat gtgcctgctt ctcttcctct ggtgggaaga aagaacgctc 1494
295 tacagagcac ttagagctta ccatgaaaat actgggagag gcagcaccta acacatgtag 1554
297 aataggactg aattattaag catggtggta tcagatgatg caaacagccc atgtcatttt 1611
299 ttttttccaga ggtagggact aataaattctc ccacactagc acctacgatc atagaacaag 1674
301 tcttttaaca catccaggag ggaaaccgct gcccaatggt ctatcccttc tctccatcc 1734
303 ctgctcaagc ccagcactgc atgtctctcc cggaaggtcc agaatgcctg tgaaatgctg 1794
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307 aa                                                                1856
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312 <212> TYPE: PRT
313 <213> ORGANISM: Rattus sp.
315 <400> SEQUENCE: 4

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320              20                  25                  30
322 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
323          35                  40                  45
325 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
326          50                  55                  60
328 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
329  65                  70                  75                  80
331 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
332              85                  90                  95
334 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
335             100                 105                 110
337 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
338             115                 120                 125
340 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
341         130                 135                 140
343 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
344 145                 150                 155                 160
347 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
348                 165                 170                 175
350 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
351             180                 185                 190
353 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
354         195                 200                 205
356 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
357     210                 215                 220
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368 <212> TYPE: DNA
369 <213> ORGANISM: Mus musculus

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<212> PRT
<213> Rattus sp.

<400> 12

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1				5					10					15	

| Val | Val | Leu | Cys | Ser | Ser | Leu | Lys | Leu | Leu | His | Tyr | Leu | Gly | Leu | Ile |
| | | | 20 | | | | 25 | | | | | 30 | | | |

| Asp | Leu | Ser | Asp | Asp | Lys | Ile | Glu | Asp | Asp | Leu | Glu | Met | Thr | Met | Val |
| | | 35 | | | | 40 | | | | | 45 | | | | |

| Cys | His | Arg | Pro | Glu | Gly | Leu | Glu | Gln | Leu | Glu | Ala | Gln | Thr | Asn | Phe |
| | 50 | | | | 55 | | | | | 60 | | | | | |

| Thr | Lys | Arg | Glu | Leu | Gln | Val | Leu | Tyr | Arg | Gly | Phe | Lys | Asn | Glu | Cys |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | |

| Pro | Ser | Gly | Val | Val | Asn | Glu | Glu | Thr | Phe | Lys | Xaa | Ile | Tyr | Ala | Gln |
| | | | 85 | | | | 90 | | | | | | 95 | | |

| Phe | Phe | Pro | His | Gly | Asp | Ala | Ser | Thr | Tyr | Ala | His | Tyr | Leu | Phe | Asn |
| | | 100 | | | | 105 | | | | | 110 | | | | |

| Ala | Phe | Asp | Thr | Thr | Gln | Thr | Gly | Ser | Val | Lys | Phe | Glu | Asp | Phe | Val |
| | | 115 | | | | 120 | | | | | 125 | | | | |

| Thr | Ala | Leu | Ser | Ile | Leu | Leu | Arg | Gly | Thr | Val | His | Glu | Lys | Leu | Lys |
| | 130 | | | | 135 | | | | | 140 | | | | | |

| Trp | Thr | Phe | Asn | Leu | Tyr | Asp | Ile | Asn | Lys | Asp | Gly | Tyr | Ile | Asn | Lys |
| 145 | | | | 150 | | | | 155 | | | | | | 160 | |

| Glu | Glu | Met | Met | Asp | Ile | Val | Lys | Ala | Ile | Tyr | Asp | Met | Met | Gly | Lys |
| | | | 165 | | | | 170 | | | | | 175 | | | |

| Tyr | Thr | Tyr | Leu | Val | Leu | Lys | Glu | Asp | Thr | Ser | Arg | Gln | His | Val | Asp |
| | | 180 | | | | 185 | | | | | 190 | | | | |

| Val | Phe | Phe | Gln | Lys | Met | Asp | Lys | Asn | Lys | Asp |
| | | 195 | | | | 200 | | | | |

see item 10
on Error
Summary
Sheet

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 10/04/2000
PATENT APPLICATION   US/09/670,756   TIME: 22:17:55

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 11
L:936 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:12
L:936 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:936 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:936 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:936 M:310 W: (46) "n" or "Xaa" used, Feature required for SEQ ID# 12
L:3028 M:311 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3362 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:3362 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
L:3362 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
L:3365 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:43
L:3365 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:43
M:340 Repeated in SeqNo=43